

ABSTRACT OF THE DISCLOSURE

[00065] This invention provides a method for rapidly obtaining accurate three-dimensional structure of proteins including large or multi-sub unit proteins, using a combination of NMR analysis of backbone only ^{13}C , ^{15}N or ^{13}C and ^{15}N isotopically labeled proteins which are optionally also ^2H isotopically labeled in the $\text{C}\alpha$ position protons and residual dipolar coupling measurements in more than one partially aligned state.